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Complete Genome Sequences of Influenza A/H1N1 Strains Isolated from Patients during the 2013-2014 Epidemic Season in Finland

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Here, we report 40 complete genome sequences of influenza A/H1N1 strains isolated from 33 nonhospitalized and 7 hospitalized patients during the 2013-2014 epidemic season in Finland. An analysis of the aligned sequences revealed no oseltamivir-resistant genotypes. As a whole, the recent viruses have drifted from the prototype A/California/7/2009 virus by ca. 1.3%.

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Influenza A viruses evolve rapidly and cause global pandemics and annual epidemics, which represent serious social and economic problems. The 2009 pandemic was caused by a novel influenza A virus of the H1N1 subtype. Since 2010, these viruses have contributed to seasonal epidemics. Approximately 20% of the general population becomes infected with these viruses, 17% of whom visit physicians. Of these patients, approximately 2% are hospitalized with more severe infections and resulting complications (1). Hospitalized patients often receive oseltamivir as an antiviral treatment.

Similarly to other influenza A viruses, the genomes of H1N1 viruses consist of 8 single-stranded RNA segments that encode 11 proteins: hemagglutinin (HA), neuraminidase (NA), nucleocapsid protein (NP), matrix (M) proteins (M1 and M2), nonstructural proteins (NS1), nuclear export protein (NEP), polymerase subunits (polymerase acidic [PA], polymerase basic 1 [PB1], and PB2), and auxiliary protein (PA-X). It was recently shown that a mutation in the NA gene of the 2009 pandemic virus (H275Y) is associated with resistance to oseltamivir (2).

Here, we collected nasopharyngeal aspirate samples from 7 hospitalized and 33 nonhospitalized patients diagnosed with influenza virus infections using reverse transcription-quantitative PCR (qRT-PCR) assays during the 2013-2014 epidemic season in Finland. The patients did not receive oseltamivir treatment before sampling. Due to a low concentration of viral RNA in some samples, we amplified the corresponding viruses in MDCK cell cultures. In total, 40 complete H1N1 genomes were sequenced using standard procedures (3). We translated the nucleotide sequences into amino acid sequences of 11 H1N1 proteins. An analysis of the aligned sequences revealed no H275Y mutation in NA associated with oseltamivir resistance. Thus, this and our previous efforts (3-5) revealed no oseltamivir-resistant genotypes in a total of 184 influenza H1N1 viruses isolated from patients from 2009 to 2014 in Finland.

Nucleotide sequence accession numbers. The full-genome sequences of influenza A viruses have been deposited in GenBank under the accession numbers [KM366535](#) to [KM366542](#), [KM437714](#) to [KM437721](#), [KM437730](#) to [KM437737](#), [KM437738](#) to [KM437745](#), [KM437746](#) to [KM437753](#), [KM366583](#) to [KM366590](#), [KM366591](#) to [KM366598](#), [KM366599](#) to [KM366606](#), [KM437754](#) to [KM437761](#), [KM437762](#) to [KM437769](#), [KM366607](#) to [KM366614](#), [KM366615](#) to [KM366622](#), [KM366639](#) to [KM366646](#), [KM366623](#) to [KM366630](#), [KM366631](#) to [KM366638](#), [KM437802](#) to [KM437809](#), [KM437810](#) to [KM437817](#), [KM437834](#) to [KM437841](#), [KM366647](#) to [KM366654](#), [KM366655](#) to [KM366662](#), [KM437850](#) to [KM437857](#), [KM366663](#) to [KM366670](#), [KM366671](#) to [KM366678](#), [KM366679](#) to [KM366686](#), [KM366703](#) to [KM366710](#), [KM366711](#) to [KM366718](#), [KM366719](#) to [KM366726](#), [KM437634](#) to [KM437641](#), [KM366727](#) to [KM366734](#), [KM366735](#) to [KM366742](#), [KM366743](#) to [KM366750](#), [KM366751](#) to [KM366758](#), [KM366759](#) to [KM366766](#), [KM366767](#) to [KM366774](#), [KM366775](#) to [KM366782](#), [KM437642](#) to [KM437649](#), [KM437650](#) to [KM437657](#), [KM3666375](#) to [KM3666382](#), [KM366455](#) to [KM366462](#), and [KM366471](#) to [KM366478](#).

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